

Rec'd PET/PTO 29 APR 2005

Docket No.: 13111-00001-US

10/521916 (LACENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Markus Matuschek et al.

Application No.: 10/521,916

Confirmation No.: N/A

Filed: January 20, 2005

Art Unit: N/A

For: PROCESS FOR THE BIOTRANSFORMATION
OF CAROTENOIDS

Examiner: Not Yet Assigned

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

MS Sequence
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

- ☐ I hereby state, in accordance with the requirements of 37 C.F.R. §1.821(f), that the information recorded in computer readable form is identical to the written Sequence Listing submitted herewith.
- ☐ I hereby state that the submission filed in accordance with 37 C.F.R. 1.821(g) does not include new matter.
- ☐ I hereby state that the submission filed in accordance with 37 C.F.R. §1.821(h) does not include new matter or go beyond the disclosure in the international application as filed.
- ☒ I hereby state that the amendments, made in accordance with 37 C.F.R. §1.825(a), included in the substitute sheet(s) of the Sequence Listing are supported in the application, as filed, in pages 1-11 of the Sequence Listing. I hereby state that the substitute sheets of the Sequence Listing do not include new matter.
- ☒ I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(b), is the same as the amended Sequence Listing.
- ☐ I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(d), contains identical data to that originally filed on January 20, 2005.

Application No.: 10/521916

Docket No.: 13111-00001-US

Dated: *April 26, 2005*

Respectfully submitted,

By *Christine M. Hansen*

Christine M. Hansen

Registration No.: 40,634

CONNOLLY BOVE LODGE & HUTZ LLP

1007 North Orange Street

P.O. Box 2207

Wilmington, Delaware 19899

(302) 658-9141

(302) 658-5614 (Fax)

Attorney for Applicant

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10/521916

SEQUENCE LISTING

<110> Matuschek, Markus
Hauer, Bernhard
Schmid, Rolf
Kauffmann, Isabelle
Blasco, Francesca
Schmidt-Dannert, Claudia

<120> Process for the biotransformation of carotenoids

<130> 13111-00001-US

<140> 10/521,916

<141> 2005-01-20

<150> PCT/EP2003/008199

<151> 2003-07-25

<150> DE 102 34 126.5

<151> 2002-07-26

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<170> PatentIn Ver. 3.3

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<212> DNA

<213> Thermus thermophilus

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Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu	
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Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg	
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Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg	
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Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu	
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<213> Thermus thermophilus

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Pro	Glu	Gly	Val	Glu	Gly	Ala	Leu	Leu	Ala	Glu	Gly	Thr	Thr	Lys	Ala	
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 130 135 140
 Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
 145 150 155 160
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 165 170 175
 Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
 180 185 190
 Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg
 195 200 205
 Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu
 210 215 220
 Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg
 225 230 235 240
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 Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe
 290 295 300
 Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly
 305 310 315 320
 Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys
 325 330 335
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<223> Description of the artificial sequence: N-terminal
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Trp Gly Arg Ala His Pro Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro	
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Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala	
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Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr	
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gag cac gcc ctt aag gcc ctg gac cgg atc atg gcc cag acc agg agc Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser 165 170 175			528
ccc ctg gcc ctc ctg gac ctg gcc gcc gaa gcc cgc ttc cgg aag gac Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp 180 185 190			576
cgg ggg gcc ctc tac cgc gag gcg gaa gcc ctc atc gtc cac ccg ccc Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro 195 200 205			624
ctc tcc cac ctt ccc cga gag cgc gcc ctg agc gag gcc gtg acc ctc Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu 210 215 220			672
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ccc gcc tgg atc ctc acc cgg agg ctg gaa agg ccc ctc ctc ctg gga Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly 275 280 285			864
gag gac cgg ctc ccc ccg ggc acc acc ctg gtc ctc tcc ccc tac gtg Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val 290 295 300			912
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ccc ttc ccc cgg gtc ctc gcc cag gtc acc ctg agg ccc gaa ggc ggg 1152
Pro Phe Pro Arg Val Leu Ala Gln Val Thr Leu Arg Pro Glu Gly Gly
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ctt ccc gcg cgg cct agg gag gag gtg cgg gcg tga 1188
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<211> 395

<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: N-terminal
his tagged

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Leu Ala Leu Ile Phe Asp Pro Glu Gly Val Glu Gly Ala Leu Leu Ala
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Glu Gly Thr Thr Lys Ala Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu
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Thr Gly Arg Gly Leu Leu Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala
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Arg Lys Ala Leu Lys Asp Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr
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Arg Glu Ala Met Glu Glu Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg
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Gly Glu Glu Arg Asp Leu Asp His Glu Met Leu Ala Leu Ser Leu Arg
130 135 140

Leu Leu Gly Arg Ala Leu Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala
145 150 155 160

Glu His Ala Leu Lys Ala Leu Asp Arg Ile Met Ala Gln Thr Arg Ser
 165 170 175
 Pro Leu Ala Leu Leu Asp Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp
 180 185 190
 Arg Gly Ala Leu Tyr Arg Glu Ala Glu Ala Leu Ile Val His Pro Pro
 195 200 205
 Leu Ser His Leu Pro Arg Glu Arg Ala Leu Ser Glu Ala Val Thr Leu
 210 215 220
 Leu Val Ala Gly His Glu Thr Val Ala Ser Ala Leu Thr Trp Ser Phe
 225 230 235 240
 Leu Leu Leu Ser His Arg Pro Asp Trp Gln Lys Arg Val Ala Glu Ser
 245 250 255
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 Pro Ala Trp Ile Leu Thr Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly
 275 280 285
 Glu Asp Arg Leu Pro Pro Gly Thr Thr Leu Val Leu Ser Pro Tyr Val
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 Thr Gln Arg Leu His Phe Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg
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 Phe Leu Glu Glu Arg Gly Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly
 325 330 335
 Leu Gly Gln Arg Leu Cys Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly
 340 345 350
 Pro Ile Val Leu Arg Ala Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu
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<223> His tag

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<223> Description of the artificial sequence: N-terminal
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cag caa gat ccc ctc gcc gtc ctg ctg gcg tgg ggc cgg gcc cac ccc	96
Gln Gln Asp Pro Leu Ala Val Leu Leu Ala Trp Gly Arg Ala His Pro	
20 25 30	
cgg ctc ttc ctt ccc ctg ccc cgc ttc ccc ctg gcc ctg atc ttt gac	144
Arg Leu Phe Leu Pro Leu Pro Arg Phe Pro Leu Ala Leu Ile Phe Asp	
35 40 45	
ccc gag ggg gtg gag ggg gcg ctc ctc gcc gag ggg acc acc aag gcc	192
Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala	
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acc ttc cag tac cgg gcc ctc tcc cgc ctc acg ggg agg ggc ctc ctc	240
Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu	
65 70 75 80	
acc gac tgg ggg gaa agc tgg aag gag gcg cgc aag gcc ctc aaa gac	288
Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp	
85 90 95	
ccc ttc ctg ccg aag aac gtc cgc ggc tac cgg gag gcc atg gag gag	336
Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu	
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Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu	
115 120 125	
gac cac gag atg ctc gcc ctc tcc ctg cgc ctc ctc ggg cgg gcc ctc	432
Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu	
130 135 140	
ttc ggg aag ccc ctc tcc cca agc ctc gcg gag cac gcc ctt aag gcc	480
Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala	

145	150	155	160	
ctg gac cgg atc atg gcc cag acc agg agc ccc ctg gcc ctc ctg gac				528
Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp				
	165	170	175	
ctg gcc gcc gaa gcc cgc ttc cgg aag gac cgg ggg gcc ctc tac cgc				576
Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg				
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gag gcg gaa gcc ctc atc gtc cac ccg ccc ctc tcc cac ctt ccc cga				624
Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg				
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gag cgc gcc ctg agc gag gcc gtg acc ctc ctg gtg gcg ggc cac gag				672
Glu Arg Ala Leu Ser Glu Ala Val Thr Leu Leu Val Ala Gly His Glu				
	210	215	220	
acg gtg gcg agc gcc ctc acc tgg tcc ttt ctc ctc ctc tcc cac cgc				720
Thr Val Ala Ser Ala Leu Thr Trp Ser Phe Leu Leu Leu Ser His Arg				
	225	230	235	240
ccg gac tgg cag aag cgg gtg gcc gag agc gag gag gcg gcc ctc gcc				768
Pro Asp Trp Gln Lys Arg Val Ala Glu Ser Glu Glu Ala Ala Leu Ala				
	245	250	255	
gcc ttc cag gag gcc ctg agg ctc tac ccc ccc gcc tgg atc ctc acc				816
Ala Phe Gln Glu Ala Leu Arg Leu Tyr Pro Pro Ala Trp Ile Leu Thr				
	260	265	270	
cgg agg ctg gaa agg ccc ctc ctc ctg gga gag gac cgg ctc ccc ccg				864
Arg Arg Leu Glu Arg Pro Leu Leu Leu Gly Glu Asp Arg Leu Pro Pro				
	275	280	285	
ggc acc acc ctg gtc ctc tcc ccc tac gtg acc cag agg ctc cac ttc				912
Gly Thr Thr Leu Val Leu Ser Pro Tyr Val Thr Gln Arg Leu His Phe				
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ccc gat ggg gag gcc ttc cgg ccc gag cgc ttc ctg gag gaa agg ggg				960
Pro Asp Gly Glu Ala Phe Arg Pro Glu Arg Phe Leu Glu Glu Arg Gly				
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acc cct tcg ggg cgc tac ttc ccc ttt ggc ctg ggg cag agg ctc tgc				1008
Thr Pro Ser Gly Arg Tyr Phe Pro Phe Gly Leu Gly Gln Arg Leu Cys				
	325	330	335	
ctg ggg cgg gac ttc gcc ctc ctc gag ggc ccc atc gtc ctc agg gcc				1056
Leu Gly Arg Asp Phe Ala Leu Leu Glu Gly Pro Ile Val Leu Arg Ala				
	340	345	350	
ttc ttc cgc cgc ttc cgc cta gac ccc ctc ccc ttc ccc cgg gtc ctc				1104
Phe Phe Arg Arg Phe Arg Leu Asp Pro Leu Pro Phe Pro Arg Val Leu				
	355	360	365	
gcc cag gtc acc ctg agg ccc gaa ggc ggg ctt ccc gcg cgg cct agg				1152
Ala Gln Val Thr Leu Arg Pro Glu Gly Gly Leu Pro Ala Arg Pro Arg				
	370	375	380	

gag gag gtg cgg gcg cat cac cat cat cat cac tga
 Glu Glu Val Arg Ala His His His His His His
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1188

<210> 6

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<212> PRT

<213> Artificial sequence

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<223> Description of the artificial sequence: C-terminal
 His-tagged

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Met Lys Arg Leu Ser Leu Arg Glu Ala Trp Pro Tyr Leu Lys Asp Leu
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 35 40 45

Pro Glu Gly Val Glu Gly Ala Leu Leu Ala Glu Gly Thr Thr Lys Ala
 50 55 60

Thr Phe Gln Tyr Arg Ala Leu Ser Arg Leu Thr Gly Arg Gly Leu Leu
 65 70 75 80

Thr Asp Trp Gly Glu Ser Trp Lys Glu Ala Arg Lys Ala Leu Lys Asp
 85 90 95

Pro Phe Leu Pro Lys Asn Val Arg Gly Tyr Arg Glu Ala Met Glu Glu
 100 105 110

Glu Ala Arg Ala Phe Phe Gly Glu Trp Arg Gly Glu Glu Arg Asp Leu
 115 120 125

Asp His Glu Met Leu Ala Leu Ser Leu Arg Leu Leu Gly Arg Ala Leu
 130 135 140

Phe Gly Lys Pro Leu Ser Pro Ser Leu Ala Glu His Ala Leu Lys Ala
 145 150 155 160

Leu Asp Arg Ile Met Ala Gln Thr Arg Ser Pro Leu Ala Leu Leu Asp
 165 170 175

Leu Ala Ala Glu Ala Arg Phe Arg Lys Asp Arg Gly Ala Leu Tyr Arg
 180 185 190

Glu Ala Glu Ala Leu Ile Val His Pro Pro Leu Ser His Leu Pro Arg

195	200	205
Glu Arg Ala Leu Ser Glu	Ala Val Thr Leu Leu Val	Ala Gly His Glu
210	215	220
Thr Val Ala Ser Ala Leu	Thr Trp Ser Phe Leu Leu Leu	Ser His Arg
225	230	235 240
Pro Asp Trp Gln Lys Arg	Val Ala Glu Ser Glu Glu Ala Ala	Leu Ala
	245	250 255
Ala Phe Gln Glu Ala Leu	Arg Leu Tyr Pro Pro Ala Trp	Ile Leu Thr
	260	265 270
Arg Arg Leu Glu Arg Pro	Leu Leu Leu Gly Glu Asp	Arg Leu Pro Pro
	275 280	285
Gly Thr Thr Leu Val Leu	Ser Pro Tyr Val Thr	Gln Arg Leu His Phe
	290 295	300
Pro Asp Gly Glu Ala Phe	Arg Pro Glu Arg Phe Leu Glu Glu	Arg Gly
305	310	315 320
Thr Pro Ser Gly Arg Tyr	Phe Pro Phe Gly Leu Gly Gln	Arg Leu Cys
	325	330 335
Leu Gly Arg Asp Phe Ala	Leu Leu Glu Gly Pro Ile Val	Leu Arg Ala
	340	345 350
Phe Phe Arg Arg Phe Arg	Leu Asp Pro Leu Pro Phe	Pro Arg Val Leu
	355	360 365
Ala Gln Val Thr Leu Arg	Pro Glu Gly Gly Leu Pro	Ala Arg Pro Arg
	370	375 380
Glu Glu Val Arg Ala His	His His His His His	His
385	390	395

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<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 7

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30

<210> 8

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<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

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30

<210> 9

<211> 42

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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42

<210> 10

<211> 42

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42

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<211> 30

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

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<210> 12

<211> 44

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: PCR primer

<400> 12

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44